

**This Page Is Inserted by IFW Operations  
and is not a part of the Official Record**

## **BEST AVAILABLE IMAGES**

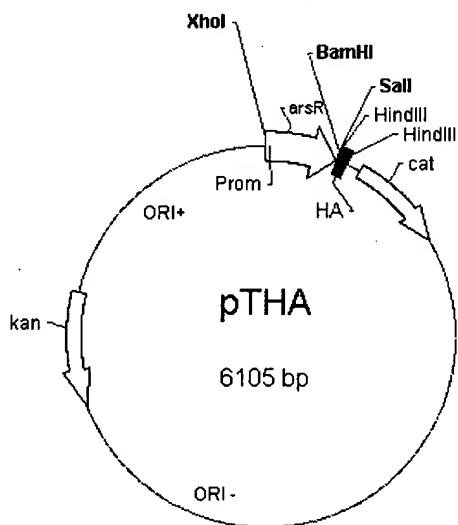
**Defective images within this document are accurate representations of the original documents submitted by the applicant.**

**Defects in the images may include (but are not limited to):**

- **BLACK BORDERS**
- **TEXT CUT OFF AT TOP, BOTTOM OR SIDES**
- **FADED TEXT**
- **ILLEGIBLE TEXT**
- **SKEWED/SLANTED IMAGES**
- **COLORED PHOTOS**
- **BLACK OR VERY BLACK AND WHITE DARK PHOTOS**
- **GRAY SCALE DOCUMENTS**

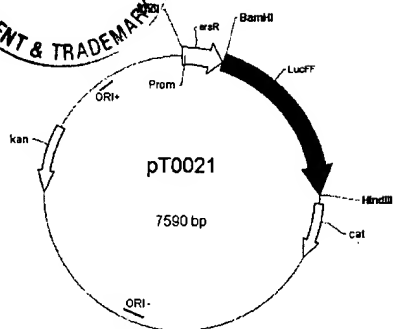
**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**



**Figure 1B**

### PCR f pT0021 with XhoF and BamHNR

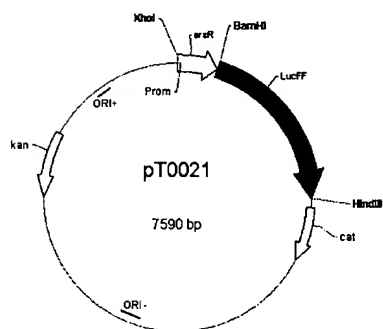


XhoF-5'-AATTCTCGAGTAAAATAACAT-3  
*XhoI*

AAATCAGGTGACTGTT**G**AGAAAAGGAGGCGGATCCCG-BamHNR  
 Stop of RBS *BamHI*  
 arsR

### Digestion with *XhoI* and *BamHI*

## Ligation



### PCR of pT0021 with LucFFB and LucFFH

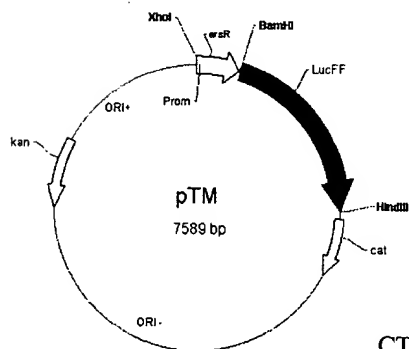
LucFFB-5'-CGGGATCCATGAGGGGTTCCGAAGACG  
*Bam*HI Start Original *Bam*HI  
of LucFF was modified

Modified between stop  
of *arsR* to *Bam*HI

GAAAGTCCAAATTGTAAGCTTGGG-LucFFH  
Stop of *HindIII*  
LucFF

### Digestion with *Bam*HI and *Hind*III

## Ligation

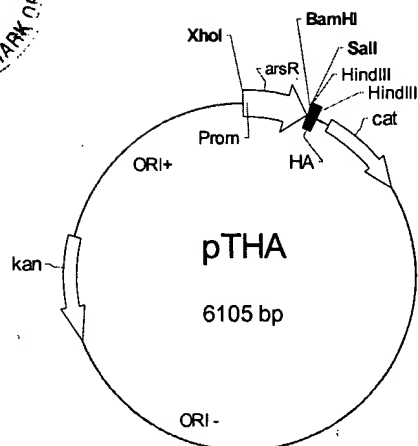


- Modified in the vicinity of *Bam*HI
- Cloning site for ORFs: *Bam*HI and *Hind*III
- No additional codons in the induced protein

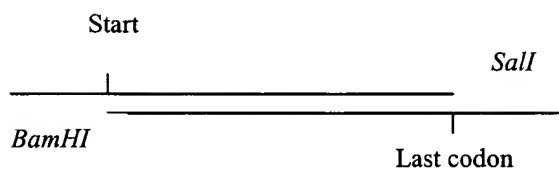




**Figure 2A**

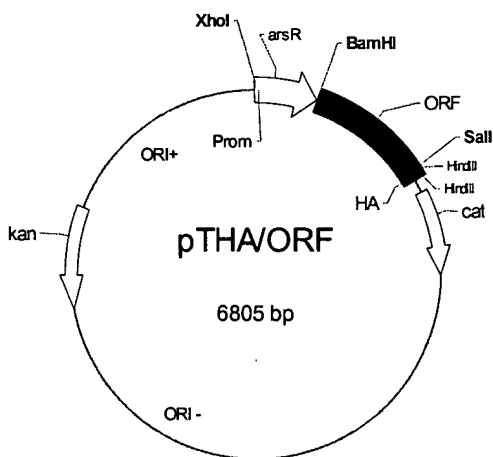


PCR of phage DNA with  
ORF specific primers

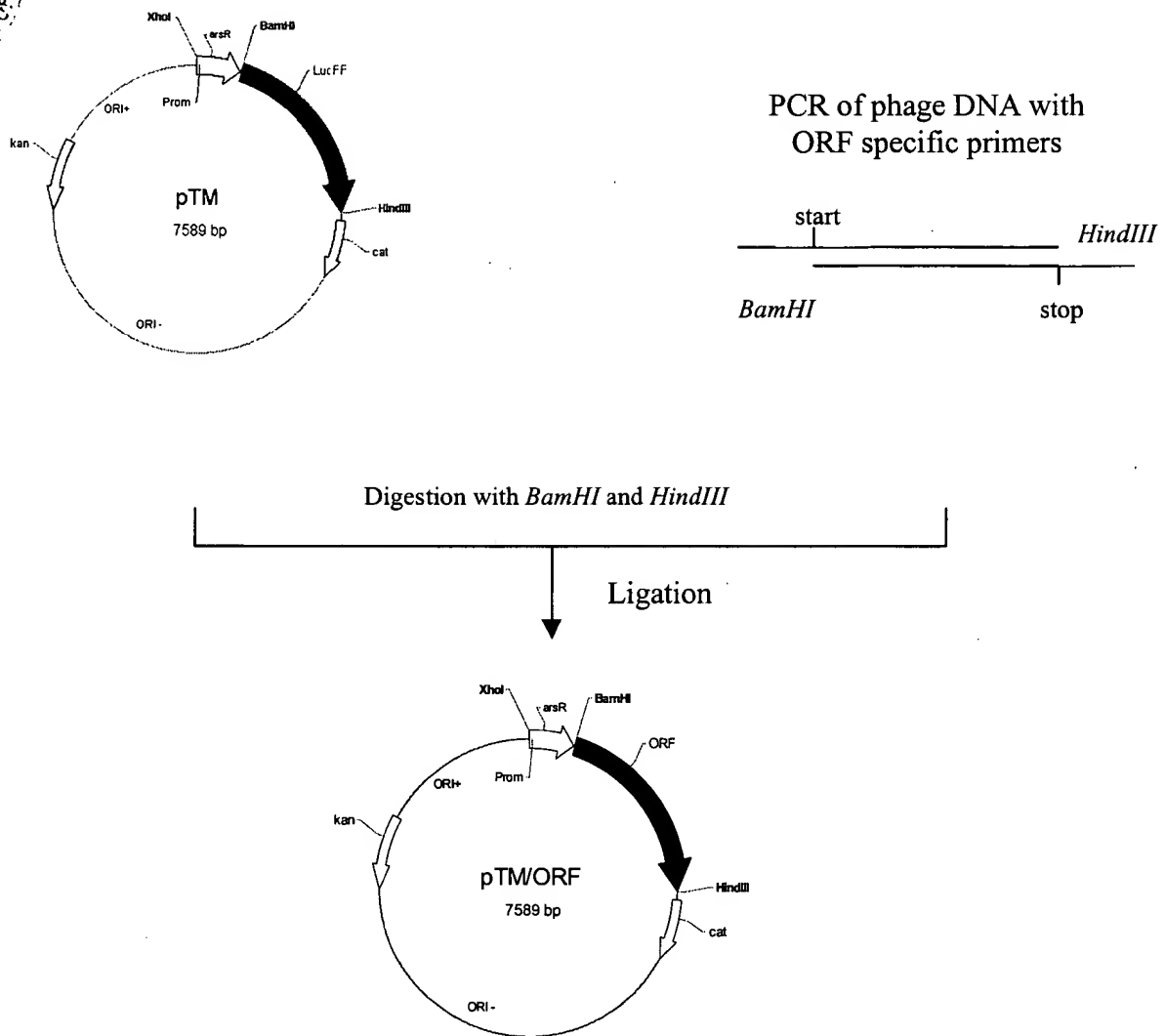


Digestion with *BamHI* and *Sall*

Ligation



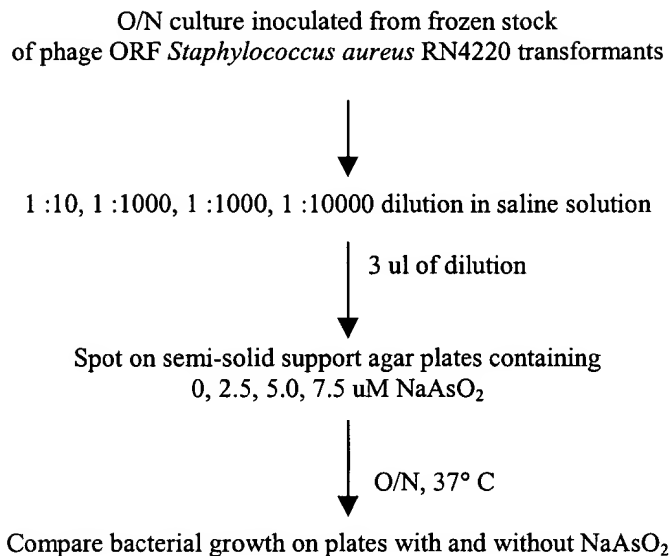
**Figure 2B**



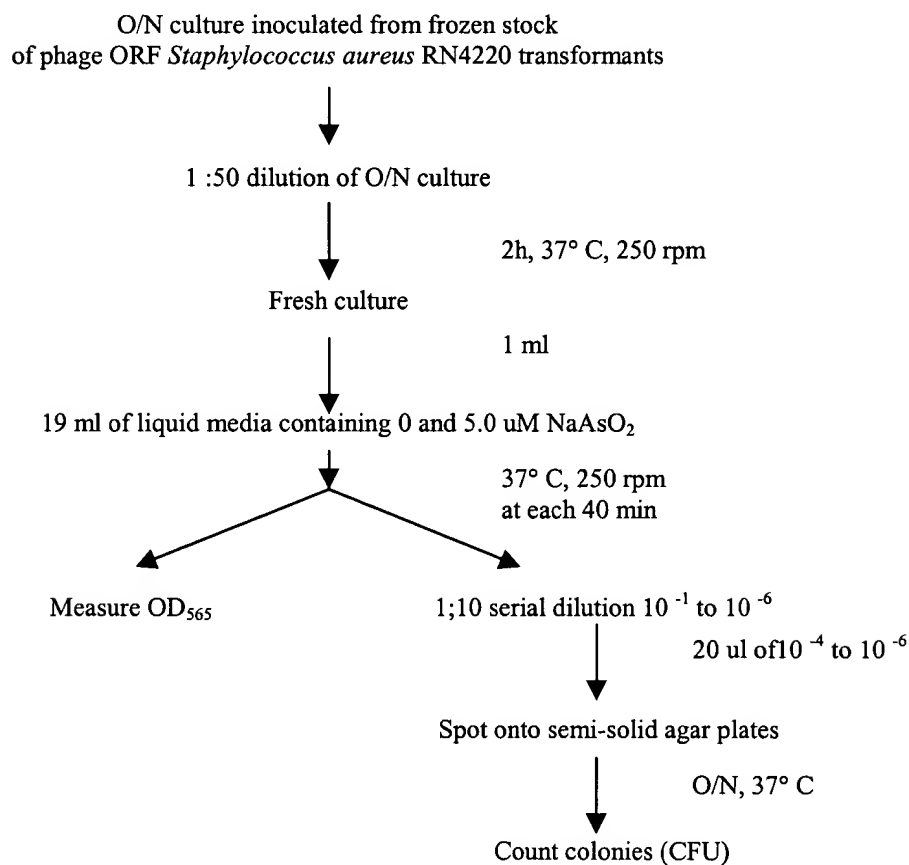


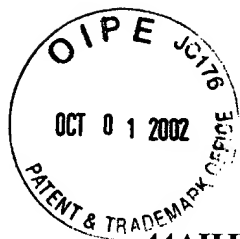
**Figure 3**

**3A: Functional assay on semi-solid support medium**



**3B: Functional assay in liquid medium**





**Figure 4A**

**44AHJD ORFs tested for functional analysis**

| UID          | POS          |
|--------------|--------------|
| 44AHJDORF001 | 12627..10342 |
| 44AHJDORF002 | 3789..5732   |
| 44AHJDORF003 | 6626..8389   |
| 44AHJDORF004 | 8764..10227  |
| 44AHJDORF005 | 13890..12643 |
| 44AHJDORF006 | 803..2029    |
| 44AHJDORF007 | 2044..3027   |
| 44AHJDORF008 | 3020..3775   |
| 44AHJDORF009 | 5744..6496   |
| 44AHJDORF010 | 14420..13938 |
| 44AHJDORF011 | 15593..15225 |
| 44AHJDORF012 | 8391..8813   |
| 44AHJDORF013 | 14996..14586 |
| 44AHJDORF019 | 9836..9630   |
| 44AHJDORF023 | 6494..6315   |
| 44AHJDORF025 | 15175..14999 |
| 44AHJDORF027 | 12916..13080 |
| 44AHJDORF028 | 9235..9071   |
| 44AHJDORF035 | 13957..13811 |
| 44AHJDORF036 | 10165..10019 |
| 44AHJDORF039 | 1743..1883   |
| 44AHJDORF040 | 9740..9877   |
| 44AHJDORF044 | 12917..12783 |
| 44AHJDORF046 | 4891..5019   |
| 44AHJDORF048 | 15340..15212 |
| 44AHJDORF049 | 5784..5909   |
| 44AHJDORF053 | 3348..3467   |
| 44AHJDORF113 | 199..600     |
| 44AHJDORF114 | 16172..15870 |
| 44AHJDORF121 | 16362..16165 |
| 44AHJDORF123 | 614..796     |



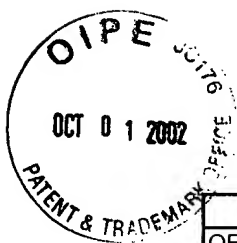
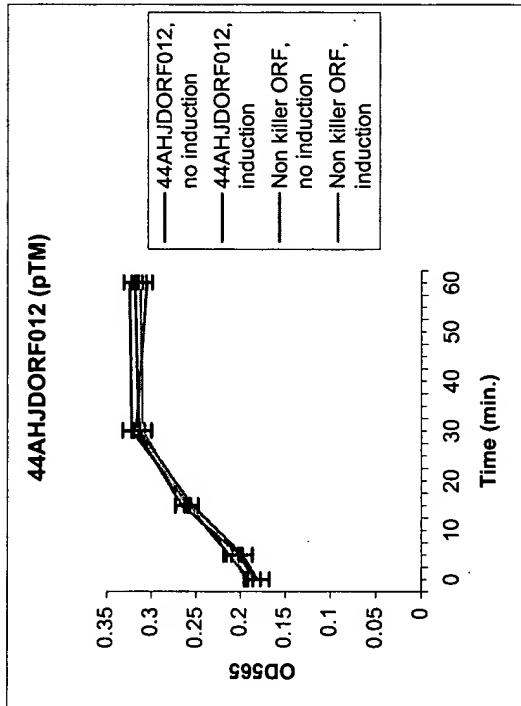


Figure 4B

| ORF ID             | <i>Staphylococcus aureus</i> transformants | Semi-solid support media |  |  |
|--------------------|--|--------------------------|--|--|
|                    |  | Without induction        |  | With induction<br>(5 uM sodium arsenite) |
| 44AHJDORF12        | Clone1                                     |                          |  |  |
|                    |  |                          |  |  |
|                    | Clone2                                     |                          |  |  |
|                    |  |                          |  |  |
|                    | Clone3                                     |                          |  |  |
|                    |  |                          |  |  |
| 44AHJDORF25        | Clone1                                     |                          |  |  |
|                    |  |                          |  |  |
|                    | Clone2                                     |                          |  |  |
|                    |  |                          |  |  |
|                    | Clone3                                     |                          |  |  |
|                    |  |                          |  |  |
| Control<br>77ORF30 | Clone1                                     |                          |  |  |
|                    |  |                          |  |  |

Figure 5A

Frame 1



Frame 2

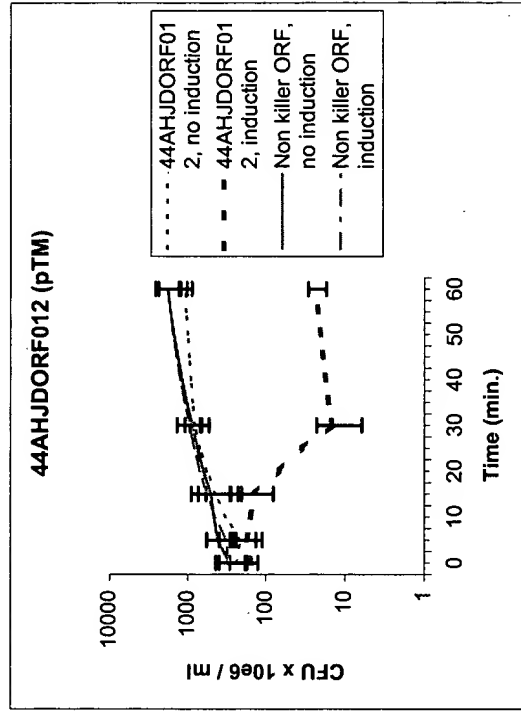
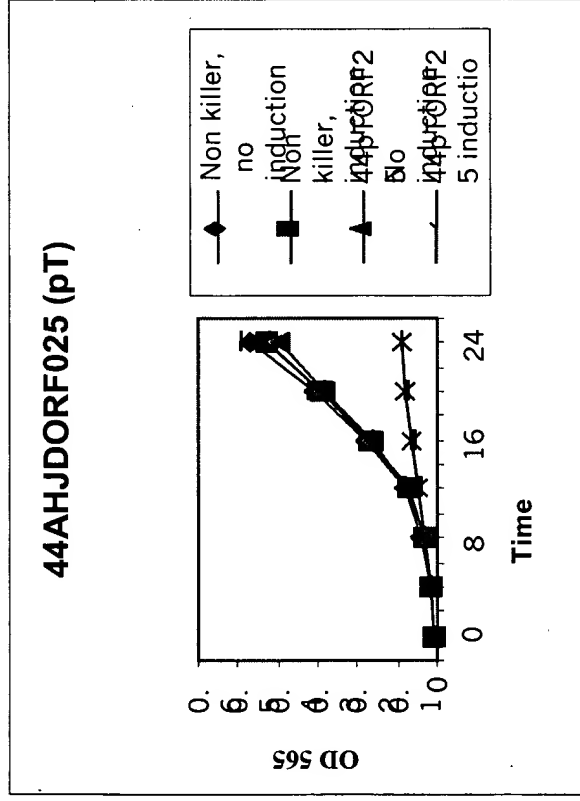
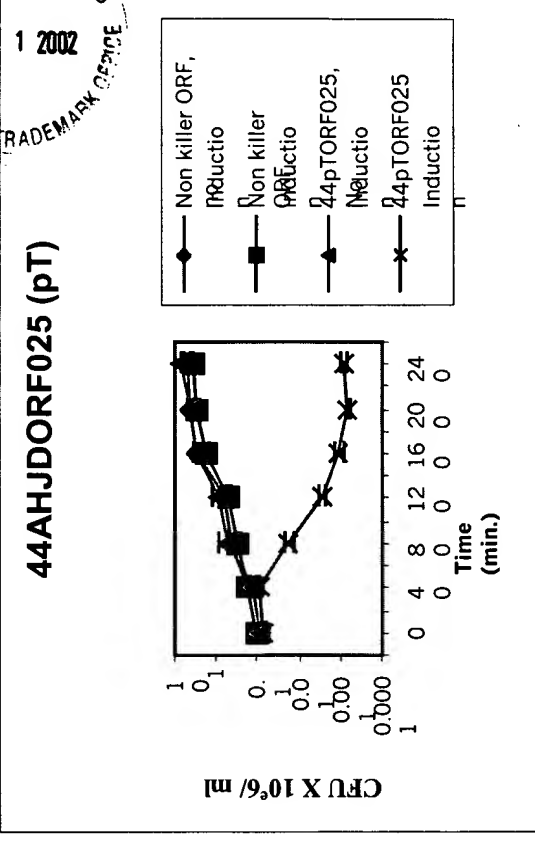


Figure 5B

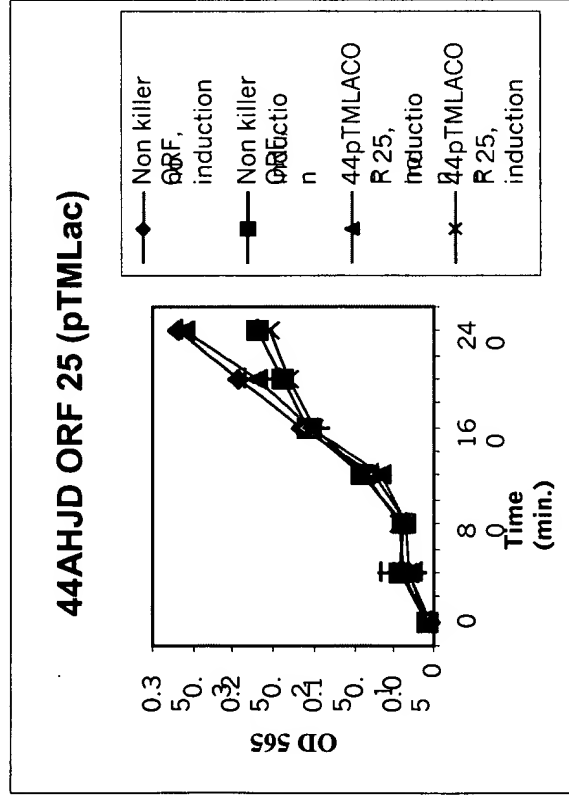
Frame 1



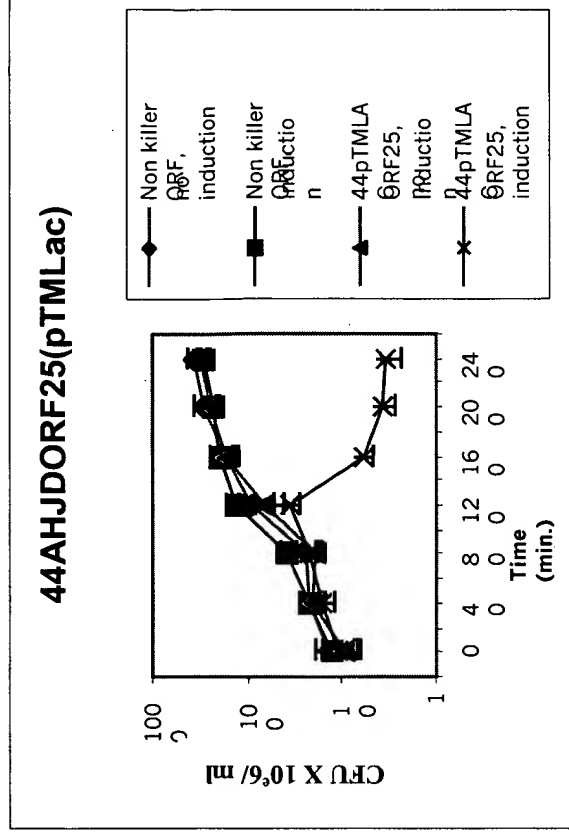
Frame 2



Frame 3



Frame 4





**FIGURE 6**

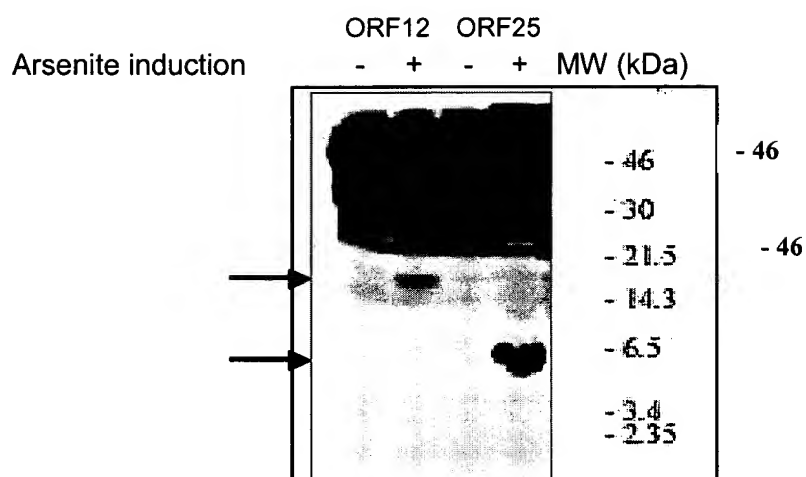
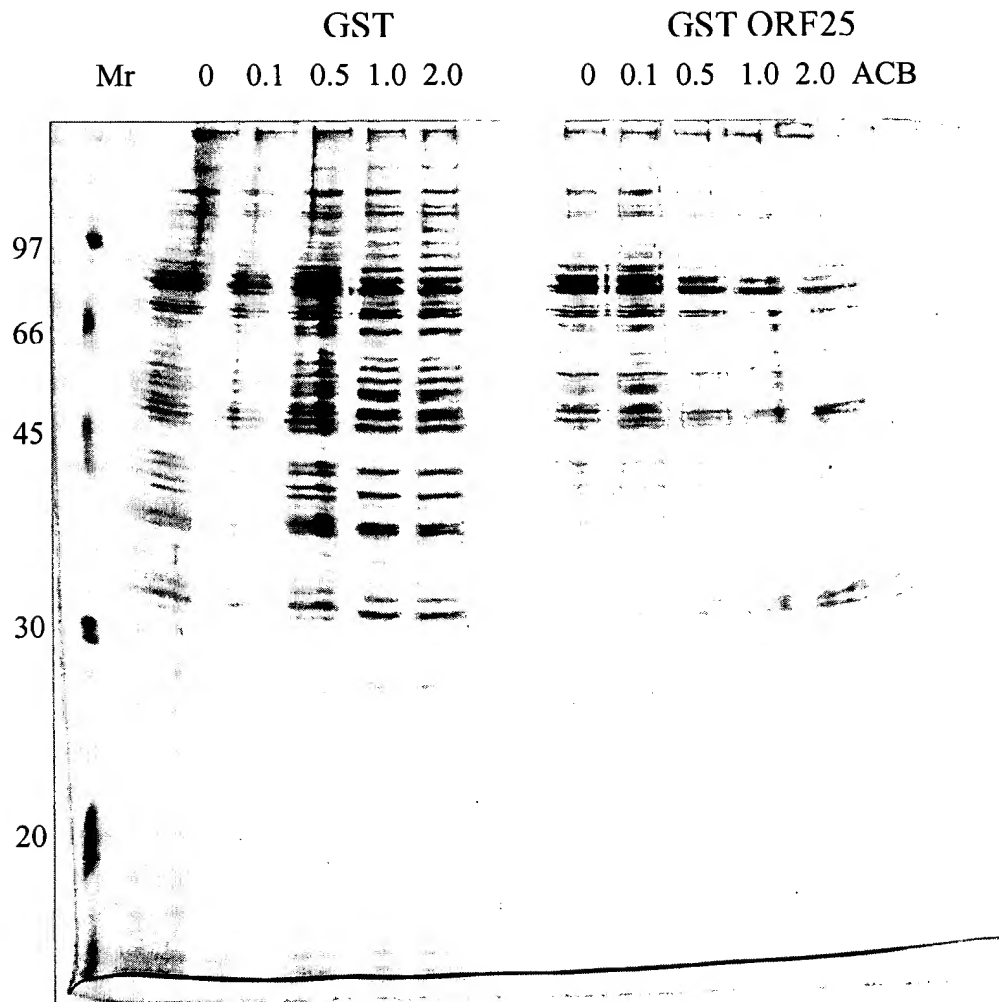


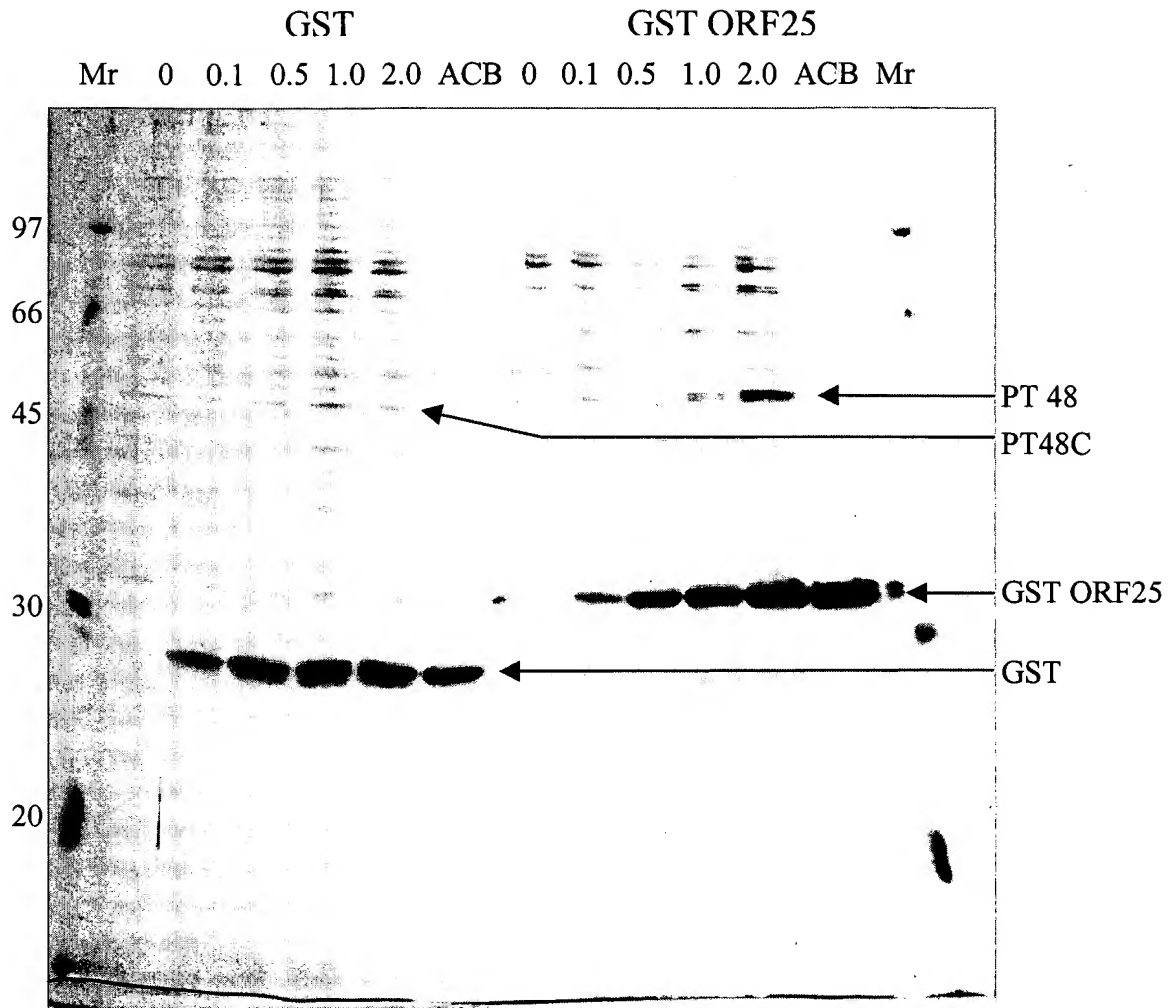


FIGURE 7A





**FIGURE 7B**



IR spectrum of compound 1. The x-axis represents wavenumber in cm⁻¹, ranging from approximately 4000 to 2500. The y-axis represents transmittance in percentage, ranging from 0 to 30000. The spectrum shows several sharp absorption bands, with the most prominent ones labeled with their wavenumbers.

| Wavenumber (cm⁻¹) |
|-------------------|
| 2701.2643         |
| 2667.2504         |
| 2475.1521         |
| 2368.1989         |
| 2321.1966         |
| 2310.2167         |
| 2289.0727         |
| 2273.2149         |
| 2185.0696         |
| 2157.1231         |
| 1990.0311         |
| 1862.8508         |
| 1752.9374         |
| 1703.9201         |
| 1642.6827         |
| 1640.7225         |
| 1549.7989         |
| 1524.8800         |
| 1517.7959         |
| 1516.7985         |
| 1492.6841         |
| 1479.7465         |
| 1426.7681         |
| 1402.6931         |
| 1301.6288         |
| 1288.6476         |
| 1202.6729         |
| 1168.5767         |
| 1152.5618         |
| 1140.5542         |
| 1066.6200         |
| 1005.5019         |
| 989.401838        |
| 971.3639          |
| 967.5156          |
| 881.4783          |



**FIGURE 9**

Details for : PT48

gil1706496|sp|P50029|DP3B\_STAAU DNA POLYMERASE III, BETA CHAIN

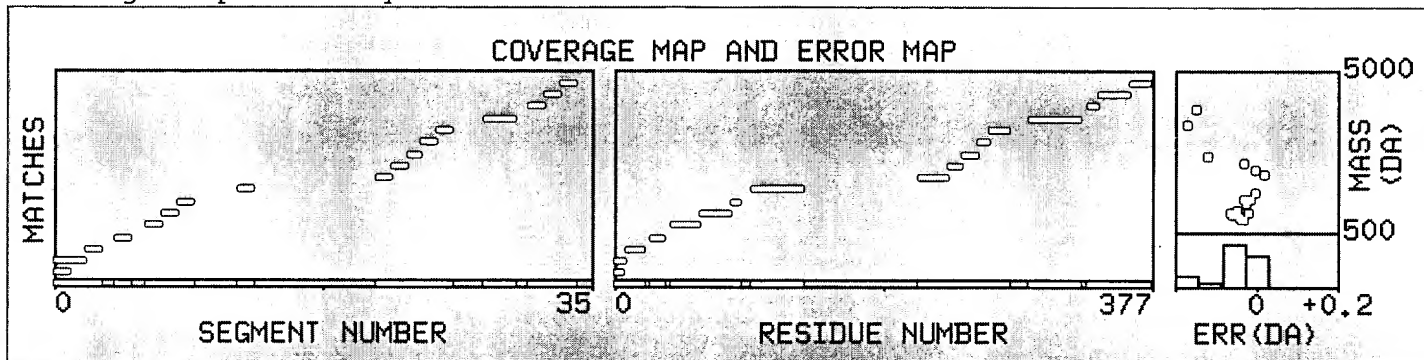
gil1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Staphylococcus aureus

Sample ID : PT 48

Number of Measured Peptides : 40

Number of Matched Peptides : 17

Coverage of protein sequence : 68%



| Measured<br>Mass(M) | Avg/<br>Mono | Computed<br>Mass | Error<br>(Da) | <u>Residues</u> |     | Missed<br>Cut | Peptide sequence                     |
|---------------------|--------------|------------------|---------------|-----------------|-----|---------------|--------------------------------------|
|                     |              |                  |               | Start           | To  |               |                                      |
| 870.370             | M            | 870.397          | -0.027        | 333             | 339 | 0             | YMDALK                               |
| 880.474             | M            | 880.505          | -0.032        | 82              | 88  | 0             | FFVDIIK                              |
| 898.392             | M            | 898.429          | -0.037        | 1               | 7   | 0             | MMEFTIK                              |
| 1004.492            | M            | 1004.540         | -0.048        | 235             | 243 | 0             | VGNVNFISR                            |
| 1054.514            | M            | 1054.530         | -0.016        | 1               | 8   | 1             | MMEFTIKR                             |
| 1055.603            | M            | 1055.658         | -0.055        | 26              | 35  | 0             | TTLPILTGIK                           |
| 1151.546            | M            | 1151.586         | -0.040        | 255             | 263 | 0             | LFPENYEIK                            |
| 1300.619            | M            | 1300.641         | -0.021        | 244             | 254 | 0             | LLEGHYPDTTR                          |
| 1425.769            | M            | 1425.782         | -0.013        | 363             | 375 | 0             | GDDSVTQLILPIR                        |
| 1469.713            | M            | 1469.740         | -0.026        | 9               | 20  | 0             | DYFITQLNDTLK                         |
| 1648.781            | M            | 1648.784         | -0.003        | 264             | 277 | 0             | LSIDNGEFYHAIDR                       |
| 2156.112            | M            | 2156.095         | 0.017         | 61              | 81  | 0             | TVDGEDIVNISETGSVVLPGR                |
| 2309.198            | M            | 2309.199         | -0.000        | 40              | 60  | 0             | EHEVILTGSDSEISIEITIPK                |
| 2474.139            | M            | 2474.166         | -0.027        | 214             | 234 | 0             | IMSDNEEDIDIFFASNQVLFK                |
| 2666.266            | M            | 2666.365         | -0.099        | 340             | 362 | 0             | AIDNDEVEVEFFGTMKPFILKPK              |
| 3577.670            | A            | 3577.809         | -0.139        | 292             | 326 | 1             | LSTGDDVVELSSTSPEIGTVKEEVDANDVEGGSLK  |
| 4033.298            | A            | 4033.421         | -0.123        | 97              | 132 | 0             | LSTNEQFQTLITSGHSEFNLSGLDPDQYPLLPQVSR |





## **FIGURE 10**

**Figure 10A : SEQ ID NO : 166**

ATGATGGAATTCACTATTAAAAGAGATTATTTTATTACACAATTAAATGACACATTAAAA  
GCTATTTACCAAGAACAACATTACCTATATTAACCTGGTATCAAAATCGATGCGAAAGAA  
CATGAAGTTATATTAACCTGGTTCAGACTCTGAAATTTCAATAGAAATCACTATTCCTAAA  
ACTGTAGATGGCGAAGATATTGTCAATATTTAGAAAACAGGCTCAGTAGTACTTCCTGGA  
CGATTCTTTGTTGATATTATAAAAAAATTACCTGGTAAAGATGTTAAATTATCTACAAAT  
GAACAATTCAGACATTAATTACATCAGGTCATTCTGAATTTAATTTAAGTGGCTTAGAT  
CCAGATCAATATCCTTTATTACCTCAAGTTTCTAGAGATGACGCAATTCAATTGTCGGTA  
AAAGTGCTTAAAAACGTGATTGCACAAACAAATTTTGCAGTGTCCACCTCAGAAAACACGC  
CCAGTACTAACTGGTGTGAAGTGGCTTATACAAGAAAATGAATTAATATGCACAGCGACT  
GACTCACACCGCTTGGCTGTAAGAAAGTTGCAGTTAGAAGATGTTTCTGAAAACAAAAAT  
GTCATCATTCCAGGTAAGGCTTTAGCTGAATTAAATAAAATTATGTCTGACAATGAAGAA  
GACATTGATATCTTCTTTGCTTCAAACCAAGTTTTATTTAAAGTTGGAAATGTGAACCTT  
ATTTCTCGATTATTAGAAGGACATTATCCTGATACAACACGTTTATTCCTGAAAACCTAT  
GAAATTAATTAAGTATAGACAATGGGGAGTTTTATCATGCGATTGATCGTGCCTCTTTA  
TTAGCGCGTGAAGGTGGTAATAACGTTATTAATTAAGTACAGGTGATGACGTTGTTGAA  
TTGTCTTCTACATCACCAGAAATTGGTACTGTAAAAGAAGAAGTTGATGCAAACGATGTT  
GAAGGTGGTAGCCTGAAAATTCATTCAACTCTAAATATATGATGGATGCTTTAAAGCA  
ATCGATAATGATGAGGTTGAAGTTGAATTCCTCGGTACAATGAAACCATTTATTCTAAAA  
CCAAAAGGTGACGACTCGGTAACGCAATTAATTTTACCAATCAGAACTTACTAA

**Figure 10B : SEQ ID NO : 167**

>gi|1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain -  
Staphylococcus aureus

MMEFTIKRDYFITQLNDTLKAISPRITLPILTGIKIDAKEHEVILTGSDSEISIEITIPKTVGDGDIVNI  
SETGSVVLPGRFFVDIIKKLPKDVKLSTNEQFQTLITSGHSEFNLSGLDPDQYPLLQVSRDDAIQLSV  
KVLKNVIAQTNFAVSTSETRPVLTVGNWLIQENELICTATDSHRLAVRKLQLEDVSENKNVIIIPGKALAE  
LNKIMSDNEEDIDIFFASNQVLFKVGNNVFISRLLEGHYPDTTRLFPENYEIKLSIDNGEFYHAIDRASL  
LAREGGNNVIKLSGDDVVELSSTSPEIGTVKEEVDANDVEGGSLKISFNKYMDALKAIIDNDEVEVEF  
FGTMKPFILKPKGDDSVTQLILPIRTY